--In an especially preferred embodiment, the protein comprises the amino acid sequence shown in SEQ ID NO:2 or SEQ ID NO:4.--

On page 3, please replace the paragraph spanning lines 1-5 with the following paragraph:

--The present invention includes variants of the protein defined above. Such variants include proteins having 50% or more overall homology with the sequence of SEQ ID NO:2. Typically the homology is 60% or more, more typically 65%, preferably 70%, more preferably 75%, even more preferably 80% or 85%, especially preferred are 90%, 95%, 98% or 99% homology.--

On page 3, please replace the paragraph spanning lines 6-12 with the following paragraph:

--Percentage homology preferably is calculated on the basis of amino acids that are identical in corresponding positions in the two sequences under consideration. Conservative substitutions are not taken into account. In calculation of percentage homology of a putative protein under investigation with the SEQ ID NO:2 or SEQ ID NO:4, if the protein under investigation has a different length, then the calculation is based on the amino acids in the portion of the molecule under investigation that overlaps with the sequence shown in SEQ ID NO:2 or SEQ ID NO:4.--

On page 3, please replace the paragraph spanning lines 21-27 with the following paragraph:

--Sequence homology (or identity) may moreover be determined using any suitable homology algorithm, using for example default parameters. Advantageously, the BLAST algorithm is employed, with parameters set to default values. The BLAST algorithm is described in detail in, for example: Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Madden, T.L., Tatusov, R.L. & Zhang, J. (1996) "Applications of network BLAST server" Meth. Enzymol. 266:131-141. ; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272; Altschul, S.F., Madden, T.L., Schääffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25:3389-3402; Karlin, S. & Altschul, S.F. (1990) "Methods for assessing the statistical significance of molecular sequence features by using general scoring schemes." Proc. Natl. Acad. Sci. USA 87:2264-2268; Karlin, S. & Altschul, S.F. (1993) "Applications and statistics for multiple high-scoring segments in molecular sequences." Proc. Natl.

Acad. Sci. USA 90:5873-5877, which are incorporated herein by reference. The search parameters are defined as follows, and are advantageously set to the defined default parameters.

On page 5, please replace the paragraph spanning lines 8-18 with the following paragraph:

--Although in the specific non-limiting example described below the ABA signalling component was obtained from *Nicotiana tabacumm* (tobacco) the present invention relates in general to an ABA signalling component. For example, ABA signalling components from dicotyledonous and monocotyledonous plants, including cereals such as wheat, barley, rice, maize and sorghum; field crops other than tobacco such as canola, sunflower, sugarbeet and cotton; fruit and vegetables. As an example, the corresponding ABA signalling component in maize may be found using reverse transcription followed by polymerase chain reaction (RT-PCR) using known techniques and primers devised from the sequences of SEQ ID NO:1. Confirmation that an ABA signalling component has been arrived at can be achieved using the assays of the present invention and described herein.--

On page 5, please replace the paragraph spanning lines 19-22 with the following paragraph:

--Using this approach we have also determined the corresponding ABA signalling component from *Arabidopsis thaliana*. The nucleic acid sequence is shown as SEQ ID NO:3 and corresponding amino acid sequence as SEQ ID NO:4. The present invention also includes variants of these sequences as defined herein.--

On page 6, please replace the paragraph spanning lines 17-25 with the following paragraph:

--Also included within the present invention are truncated proteins derivable from the proteins defined above. Typically such truncated proteins will be able to compete with the non-truncated protein in an ABA signalling pathway, and/or be capable of giving rise to antibodies to the non-truncated protein. Examples of such truncated proteins include Sp1 comprising amino acids 115-127 of SEQ ID NO:2 and Sp2 comprising amino acids 1-279 of SEQ ID NO:2. Thus, the present invention further includes a method of raising immunoglobins comprising administering a protein of the present invention to a mammal, such as a rabbit or human, and optionally isolating the immunoglobins generated.--

On page 6, please replace the paragraph spanning lines 28-30 with the following paragraph:

--In particular, according to another aspect of the present invention there is provided nucleic acid comprising the sequence from positions 18 to 917 shown in SEQ ID NO:1, or from positions 77 to 991 shown in SEQ ID NO:3.--

On page 17, please replace the paragraph spanning lines 21-22 with the following paragraph:

--Figure 40 (or SEQ ID NO:5) shows the antisense cDNA SYR cloned into pG3SA;--

On page 78, please replace the paragraph spanning lines 10-12 with the following paragraph:

--Sequence homology searches were performed at the BLAST sequence similarity service, provided by NCBI (National Centre for Biotechnology Information, described in detail previously herein).--

On page 111, please replace the paragraph spanning lines 7-20 with the following paragraph:

--Originally three leaves of three different plants were infiltrated with pGSA, the construct containing the antisense cDNA of *syr* (Fig. 40; SEQ ID NO:3) under the control of the 35S promoter. After three days of incubation at 23 C and 100% humidity, the plants were tested for different wilty phenotype in the leaves. The plants with soil were transferred from their 100% humidity environment to a dry place 30 cm under 180 W lamps. The leaves transformed with the pGSA seem to start wilting sooner than the control non-infiltrated leaves. This means that after approximately 5 min, the tip and edges (where the pGSA was infiltrated) of the transformed leaf were starting to hang down and being wilty, whereas the other leaves only started to dry out at approximately 10 min after the transfer. This was recorded for two of the three plants. The two transformed leaves were tested for GUS activity. Blue stains as result of the GUS activity were detected in approximately 10% of the cells in the infiltrated area, indicating gene expression via the 35S promoter was occurring in the plant cells. No GUS activity was detected in two control leaves tested.--

IN THE CLAIMS:

Please cancel Claims 3, 21-56, without prejudice to or disclaimer of the subject matter therein.

Please amend Claims 1, 2 and 4-20 as follows, without prejudice to or disclaimer of the subject matter therein. Please add new Claims 57-65.